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#5

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/899,429

DATE: 10/09/2001

TIME: 09:32:34

Input Set : A:\98385Jseq.txt

Output Set: N:\CRF3\10092001\I899429.raw

3 <110> APPLICANT: Hauptmann, Rudolph  
4 Himmeler, Adolph  
5 Maurer-Fogy, Ingrid  
6 Stratowa, Christian  
8 <120> TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNA Binding for  
9 Them  
11 <130> FILE REFERENCE: 98,385-J  
13 <140> CURRENT APPLICATION NUMBER: 09/899,429  
14 <141> CURRENT FILING DATE: 2001-07-03  
16 <150> PRIOR APPLICATION NUMBER: 09/792,356  
17 <151> PRIOR FILING DATE: 2000-02-23  
19 <150> PRIOR APPLICATION NUMBER: 08/477,639  
20 <151> PRIOR FILING DATE: 1955-06-07  
22 <150> PRIOR APPLICATION NUMBER: 08/383,676  
23 <151> PRIOR FILING DATE: 1995-02-01  
25 <150> PRIOR APPLICATION NUMBER: 08/153,287  
26 <151> PRIOR FILING DATE: 1993-11-17  
28 <150> PRIOR APPLICATION NUMBER: 07/821,750  
29 <151> PRIOR FILING DATE: 1992-01-02  
31 <150> PRIOR APPLICATION NUMBER: 07/511,430  
32 <151> PRIOR FILING DATE: 1990-04-20  
34 <160> NUMBER OF SEQ ID NOS: 87  
36 <170> SOFTWARE: PatentIn Ver. 2.0  
38 <210> SEQ ID NO: 1  
39 <211> LENGTH: 1368  
40 <212> TYPE: DNA  
41 <213> ORGANISM: Homo sapiens  
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44 <221> NAME/KEY: CDS  
45 <222> LOCATION: (1)..(1368)  
47 <220> FEATURE:  
48 <221> NAME/KEY: sig\_peptide  
49 <222> LOCATION: (1)..(87)  
51 <220> FEATURE:  
52 <221> NAME/KEY: misc\_feature  
53 <222> LOCATION: (88)..(120)  
54 <223> OTHER INFORMATION: Portion of TNF-BP pro protein cleaved by  
55 extracellular proteases following secretion.  
57 <220> FEATURE:  
58 <221> NAME/KEY: misc\_feature  
59 <222> LOCATION: (606)..(633)  
60 <223> OTHER INFORMATION: Portion of TNF-BP pro protein cleaved by  
61 extracellular proteases following secretion.  
63 <400> SEQUENCE: 1  
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65 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu  
66 1 5 10 15

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68 gag ctg ttg gtg gga ata tac ccc tca ggg gtt att gga ctg gtc cct 96
69 Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
70          20          25          30
72 cac cta ggg gac agg gag aag aga gat agt gtg tgt ccc caa gga aaa 144
73 His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
74          35          40          45
76 tat atc cac cct caa aat aat tcg att tgc tgt acc aag tgc cac aaa 192
77 Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
78          50          55          60
80 gga acc tac ttg tac aat gac tgt cca ggc ccg ggg cag gat acg gac 240
81 Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
82 65          70          75          80
84 tgc agg gag tgt gag agc ggc tcc ttc acc gct tca gaa aac cac ctc 288
85 Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
86          85          90          95
88 aga cac tgc ctc agc tgc tcc aaa tgc cga aag gaa atg ggt cag gtg 336
89 Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
90          100          105          110
92 gag atc tct tct tgc aca gtg gac cgg gac acc gtg tgt ggc tgc agg 384
93 Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
94          115          120          125
96 aag aac cag tac cgg cat tat tgg agt gaa aac ctt ttc cag tgc ttc 432
97 Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe
98          130          135          140
100 aat tgc agc ctc tgc ctc aat ggg acc gtg cac ctc tcc tgc cag gag 480
101 Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
102 145          150          155          160
104 aaa cag aac acc gtg tgc acc tgc cat gca ggt ttc ttt cta aga gaa 528
105 Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
106          165          170          175
108 aac gag tgt gtc tcc tgt agt aac tgt aag aaa agc ctg gag tgc acg 576
109 Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr
110          180          185          190
112 aag ttg tgc cta ccc cag att gag aat gtt aag ggc act gag gac tca 624
113 Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser
114          195          200          205
116 ggc acc aca gtg ctg ttg ccc ctg gtc att ttc ttt ggt ctt tgc ctt 672
117 Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu
118          210          215          220
120 tta tcc ctc ctc ttc att ggt tta atg tat cgc tac caa cgg tgg aag 720
121 Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
122 225          230          235          240
124 tcc aag ctc tac tcc att gtt tgt ggg aaa tcg aca cct gaa aaa gag 768
125 Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu
126          245          250          255
128 ggg gag ctt gaa gga act act act aag ccc ctg gcc cca aac cca agc 816
129 Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser
130          260          265          270
132 ttc agt ccc act cca ggc ttc acc ccc acc ctg ggc ttc agt ccc gtg 864

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133 Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val
134      275      280      285
136 ccc agt tcc acc ttc acc tcc agc tcc acc tat acc ccc ggt gac tgt 912
137 Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys
138      290      295      300
140 ccc aac ttt gcg gct ccc cgc aga gag gtg gca cca ccc tat cag ggg 960
141 Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
142 305      310      315      320
144 gct gac ccc atc ctt gcg aca gcc ctc gcc tcc gac ccc atc ccc aac 1008
145 Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn
146      325      330      335
148 ccc ctt cag aag tgg gag gac agc gcc cac aag cca cag agc cta gac 1056
149 Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp
150      340      345      350
152 act gat gac ccc gcg acg ctg tac gcc gtg gtg gag aac gtg ccc ccg 1104
153 Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro
154      355      360      365
156 ttg cgc tgg aag gaa ttc gtg cgg cgc cta ggg ctg agc gac cac gag 1152
157 Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu
158      370      375      380
160 atc gat cgg ctg gag ctg cag aac ggg cgc tgc ctg cgc gag gcg caa 1200
161 Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
162 385      390      395      400
164 tac agc atg ctg gcg acc tgg agg cgg cgc acg ccg cgg cgc gag gcc 1248
165 Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala
166      405      410      415
168 acg ctg gag ctg ctg gga cgc gtg ctc cgc gac atg gac ctg ctg ggc 1296
169 Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
170      420      425      430
172 tgc ctg gag gac atc gag gag gcg ctt tgc ggc ccc gcc gcc ctc ccg 1344
173 Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro
174      435      440      445
176 ccc gcg ccc agt ctt ctc aga tga 1368
177 Pro Ala Pro Ser Leu Leu Arg
178      450      455
181 <210> SEQ ID NO: 2
182 <211> LENGTH: 455
183 <212> TYPE: PRT
184 <213> ORGANISM: Homo sapiens
186 <400> SEQUENCE: 2
187 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu
188 1 5 10 15
190 Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
191 20 25 30
193 His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
194 35 40 45
196 Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
197 50 55 60
199 Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| 200 | 65  |     |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80 |
| 202 | Cys | Arg | Glu | Cys | Glu | Ser | Gly | Ser | Phe | Thr | Ala | Ser | Glu | Asn | His | Leu |    |
| 203 |     |     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |    |
| 205 | Arg | His | Cys | Leu | Ser | Cys | Ser | Lys | Cys | Arg | Lys | Glu | Met | Gly | Gln | Val |    |
| 206 |     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |    |
| 208 | Glu | Ile | Ser | Ser | Cys | Thr | Val | Asp | Arg | Asp | Thr | Val | Cys | Gly | Cys | Arg |    |
| 209 |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |    |
| 211 | Lys | Asn | Gln | Tyr | Arg | His | Tyr | Trp | Ser | Glu | Asn | Leu | Phe | Gln | Cys | Phe |    |
| 212 |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |    |
| 214 | Asn | Cys | Ser | Leu | Cys | Leu | Asn | Gly | Thr | Val | His | Leu | Ser | Cys | Gln | Glu |    |
| 215 | 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |    |
| 217 | Lys | Gln | Asn | Thr | Val | Cys | Thr | Cys | His | Ala | Gly | Phe | Phe | Leu | Arg | Glu |    |
| 218 |     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |    |
| 220 | Asn | Glu | Cys | Val | Ser | Cys | Ser | Asn | Cys | Lys | Lys | Ser | Leu | Glu | Cys | Thr |    |
| 221 |     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |    |
| 223 | Lys | Leu | Cys | Leu | Pro | Gln | Ile | Glu | Asn | Val | Lys | Gly | Thr | Glu | Asp | Ser |    |
| 224 |     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |    |
| 226 | Gly | Thr | Thr | Val | Leu | Leu | Pro | Leu | Val | Ile | Phe | Phe | Gly | Leu | Cys | Leu |    |
| 227 |     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |    |
| 229 | Leu | Ser | Leu | Leu | Phe | Ile | Gly | Leu | Met | Tyr | Arg | Tyr | Gln | Arg | Trp | Lys |    |
| 230 | 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |    |
| 232 | Ser | Lys | Leu | Tyr | Ser | Ile | Val | Cys | Gly | Lys | Ser | Thr | Pro | Glu | Lys | Glu |    |
| 233 |     |     |     | 245 |     |     |     |     |     | 250 |     |     |     | 255 |     |     |    |
| 235 | Gly | Glu | Leu | Glu | Gly | Thr | Thr | Thr | Lys | Pro | Leu | Ala | Pro | Asn | Pro | Ser |    |
| 236 |     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |    |
| 238 | Phe | Ser | Pro | Thr | Pro | Gly | Phe | Thr | Pro | Thr | Leu | Gly | Phe | Ser | Pro | Val |    |
| 239 |     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |    |
| 241 | Pro | Ser | Ser | Thr | Phe | Thr | Ser | Ser | Ser | Thr | Tyr | Thr | Pro | Gly | Asp | Cys |    |
| 242 |     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |    |
| 244 | Pro | Asn | Phe | Ala | Ala | Pro | Arg | Arg | Glu | Val | Ala | Pro | Pro | Tyr | Gln | Gly |    |
| 245 | 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |    |
| 247 | Ala | Asp | Pro | Ile | Leu | Ala | Thr | Ala | Leu | Ala | Ser | Asp | Pro | Ile | Pro | Asn |    |
| 248 |     |     |     | 325 |     |     |     |     |     | 330 |     |     |     | 335 |     |     |    |
| 250 | Pro | Leu | Gln | Lys | Trp | Glu | Asp | Ser | Ala | His | Lys | Pro | Gln | Ser | Leu | Asp |    |
| 251 |     |     | 340 |     |     |     |     |     | 345 |     |     |     | 350 |     |     |     |    |
| 253 | Thr | Asp | Asp | Pro | Ala | Thr | Leu | Tyr | Ala | Val | Val | Glu | Asn | Val | Pro | Pro |    |
| 254 |     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |    |
| 256 | Leu | Arg | Trp | Lys | Glu | Phe | Val | Arg | Arg | Leu | Gly | Leu | Ser | Asp | His | Glu |    |
| 257 |     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |    |
| 259 | Ile | Asp | Arg | Leu | Glu | Leu | Gln | Asn | Gly | Arg | Cys | Leu | Arg | Glu | Ala | Gln |    |
| 260 | 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |    |
| 262 | Tyr | Ser | Met | Leu | Ala | Thr | Trp | Arg | Arg | Arg | Thr | Pro | Arg | Arg | Glu | Ala |    |
| 263 |     |     |     | 405 |     |     |     |     |     | 410 |     |     |     | 415 |     |     |    |
| 265 | Thr | Leu | Glu | Leu | Leu | Gly | Arg | Val | Leu | Arg | Asp | Met | Asp | Leu | Leu | Gly |    |
| 266 |     |     | 420 |     |     |     |     |     | 425 |     |     |     | 430 |     |     |     |    |
| 268 | Cys | Leu | Glu | Asp | Ile | Glu | Glu | Ala | Leu | Cys | Gly | Pro | Ala | Ala | Leu | Pro |    |
| 269 |     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |    |
| 271 | Pro | Ala | Pro | Ser | Leu | Leu | Arg |     |     |     |     |     |     |     |     |     |    |
| 272 |     | 450 |     |     |     |     | 455 |     |     |     |     |     |     |     |     |     |    |

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Input Set : A:\98385Jseq.txt

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276 <211> LENGTH: 483
277 <212> TYPE: DNA
278 <213> ORGANISM: Homo sapiens
280 <220> FEATURE:
281 <221> NAME/KEY: CDS
282 <222> LOCATION: (1)..(483)
284 <400> SEQUENCE: 3
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287   1           5           10           15
289 att tgc tgt acc aag tgc cac aaa gga acc tac ttg tac aat gac tgt      96
290 Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys
291           20           25           30
293 cca ggc ccg ggg cag gat acg gac tgc agg gag tgt gag agc ggc tcc      144
294 Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser
295   35           40           45
297 ttc acc gct tca gaa aac cac ctc aga cac tgc ctc agc tgc tcc aaa      192
298 Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys
299   50           55           60
301 tgc cga aag gaa atg ggt cag gtg gag atc tct tct tgc aca gtg gac      240
302 Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp
303  65           70           75           80
305 cgg gac acc gtg tgt ggc tgc agg aag aac cag tac cgg cat tat tgg      288
306 Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp
307           85           90           95
309 agt gaa aac ctt ttc cag tgc ttc aat tgc agc ctc tgc ctc aat ggg      336
310 Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly
311   100          105          110
313 acc gtg cac ctc tcc tgc cag gag aaa cag aac acc gtg tgc acc tgc      384
314 Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys
315   115          120          125
317 cat gca ggt ttc ttt cta aga gaa aac gag tgt gtc tcc tgt agt aac      432
318 His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn
319   130          135          140
321 tgt aag aaa agc ctg gag tgc acg aag ttg tgc cta ccc cag att gag      480
322 Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu
323 145          150          155          160
325 aat                                                                 483
326 Asn
329 <210> SEQ ID NO: 4
330 <211> LENGTH: 161
331 <212> TYPE: PRT
332 <213> ORGANISM: Homo sapiens
334 <400> SEQUENCE: 4
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336   1           5           10           15
338 Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys
339   20           25           30

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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/899,429

DATE: 10/09/2001

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Output Set: N:\CRF3\10092001\I899429.raw

L:690 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:818 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:850 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:888 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:1422 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:1442 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19  
L:1488 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:1554 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26  
L:1629 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31  
L:1670 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33  
L:1673 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33  
L:1692 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34  
L:1695 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34  
L:1728 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36